

IN THE CLAIMS

Please amend the claims as follows:

Claims 1-15 (Cancelled).

Claim 16. A system for searching for relationships between base sequences in genes, comprising:

an amplified sequence recognizing portion;

a theoretical value calculating portion;

a comparing portion; and

a displaying portion;

wherein said amplified sequence recognizing portion

reads pre-amplification base sequence data of known genes, and

produces, based on primer data including name, identification number, and

recognition site data of the primers used for amplifying base sequences, and

allowance limit for mismatch of predetermined forward and reverse primer; post-amplification base sequence data,

wherein said post-amplification base sequence data comprises one or more of names of the primers, identification numbers of the primers, DNA number, group of the base sequences, name of organisms, and name of the known gene;

wherein said theoretical value calculation portion

calculates, based on input data stored in a restriction enzyme database,

theoretical restriction fragment length values of the known genes digested by restriction enzymes, and the post-amplification base sequence data, and

outputs theoretical restriction fragment pattern data,

wherein said input data comprises sequence of the known genes, restriction enzyme data comprising a set of the name and identification number of restriction enzymes, recognition sites recognized by the restriction enzymes, and restriction sites at which the restriction enzymes cut in the recognition sites,

wherein said theoretical restriction fragment pattern data comprises at least said post-amplification base sequence data, said theoretical restriction fragment length values, and numerical value which is 1 for theoretical data, or 2 for measured data;

wherein said comparing portion

compares the theoretical restriction fragment pattern data with measured restriction fragment pattern data,

calculates the degree of similarity of the known genes to the sample, and outputs said degree of similarity to said displaying portion,

wherein said measured restriction fragment pattern data comprises a name or identification number of the restriction enzymes, measured restriction fragment length values obtained as a result of digesting a sample with the restriction enzymes followed by measurement and at least one name or identification number of the primers;

wherein said displaying portion diagrammatically displays samples having a similarity therebetween based on the calculation of the degree of similarity, or displays a set of a known gene and a sample having similarity therebetween based on the calculation of the degree of similarity.

Claim 17. (New) The system as claimed in claim 16, wherein the displaying portion diagrammatically displays samples having a similarity therebetween based on the the calculation of the degree of similarity, or displays a set of a known gene and a sample having

similarity therebetween based on the calculation of the degree of similarity by a dendrogram.

Claim 18. (New) The system as claimed in claim 16, wherein the comparing portion calculates the degree of similarity based on the theoretical restriction fragment patterns and the measured restriction fragment patterns with a weighted-pair-group method with arithmetic mean.

Claim 19. (New) A method of searching for relationship between base sequences in genes, comprising steps of

reading pre-amplification base sequence data of known genes; and  
producing, based on primer data including name, identification number, and  
recognition site data of the primers used for amplifying base sequences, and allowance limit  
for mismatch of predetermined forward and reverse primer; post-amplification base sequence  
data,

wherein the post-amplification base sequence data comprises one or more of names  
of the primers, identification numbers of the primers, DNA number, Group of the base  
sequences, name of organisms, and name of the known gene;

steps of

calculating, based on input data stored in a restriction enzyme database, theoretical  
restriction fragment length values of the known genes digested by restriction enzymes, and  
the post amplification base sequence data; and

outputting theoretical restriction fragment pattern data,

wherein said input data comprises sequences of the known genes, restriction enzyme  
data comprising a set of name and identification number of restriction enzymes, recognition

sites recognized by the restriction enzymes, and restriction sites at which the restriction enzymes cut in the recognition sites, and

wherein said theoretical restriction fragment pattern data comprises at least said post amplification base sequence data, said theoretical restriction fragment length values, and numerical value which is 1 for theoretical data, or 2 for measured data;

steps of

comparing the theoretical restriction fragment pattern data with measured restriction fragment pattern data;

calculating the degree of similarity of the known genes to the sample; and

outputting said degree of similarity to a display

wherein the measured restriction fragment pattern data comprises a name or identification number of the restriction enzymes, measured restriction fragment length values obtained as a result of digesting a sample with the restriction enzymes followed by measurement and at least one name or identification number of the primers; and

a step of diagrammatically displaying samples having a similarity therebetween based on the calculation of the degree of similarity, or displaying a set of a known gene and a sample having similarity therebetween based on the calculation of the degree of similarity.

Claim 20. (New) The method as claimed in claim 19, wherein the diagrammatically displaying comprises displaying a dendrogram.

Claim 21. (New) The method as claimed in claim 19, wherein the comparing comprises an unweighted-pair-group method with arithmetic mean.

Claim 22. (New) A recording medium readable on a computer having recorded therein a computer program for implementing:

steps of

reading pre-amplification base sequence data of known genes; and  
producing, based on primer data including name, identification number, and  
recognition site data of the primers used for amplifying base sequences, and allowance limit  
for mismatch of predetermined forward and reverse primer; post-amplification base sequence  
data,

wherein the post-amplification base sequence data comprises one or more of names  
of the primers, identification numbers of the primers, DNA number, Group of the base  
sequences, name of organisms, and name of the known gene;

steps of

calculating, based on input data stored in a restriction enzyme database, theoretical  
restriction fragment length values of known genes digested by restriction enzymes, and the  
post amplification base sequence data; and

outputting theoretical restriction fragment pattern data,

wherein said input data comprises sequences of the known genes, restriction enzyme  
data comprising a set of name and identification number of restriction enzymes, recognition  
sites recognized by the restriction enzymes, and restriction sites at which the restriction  
enzymes cut in the recognition sites, and

wherein said theoretical restriction fragment pattern data comprises at least said post  
amplification base sequence data, said theoretical restriction fragment length values, and  
numerical value which is 1 for theoretical data, or 2 for measured data;

steps of

comparing the theoretical restriction fragment pattern data with measured restriction fragment pattern data;

calculating the degree of similarity of the known genes to the sample; and

outputting said degree of similarity to a display

wherein the measured restriction fragment pattern data comprises a name or identification number of the restriction enzymes, measured restriction fragment length values obtained as a result of digesting a sample with the restriction enzymes followed by measurement and at least one name or identification number of the primers; and

a step of diagrammatically displaying samples having a similarity therebetween based on the calculation of the degree of similarity, or displaying a set of a known gene and a sample having similarity therebetween based on the calculation of the degree of similarity.

Claim 23. (New) The recording medium as claimed in claim 22, wherein the displaying step diagrammatically displays samples having a similarity therebetween based on the calculation of the degree of similarity, or displays a set of a known gene and a sample having similarity therebetween based on the calculation of the degree of similarity by a dendrogram.

Claim 24. (New) The recording medium as claimed in claim 22, wherein the comparing step calculates the degree of similarity based on the theoretical restriction fragment patterns and the measured restriction fragment patterns with a weighted-pair-group method with arithmetic mean.